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============================================================
Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Thu Sep 27 13:54:46 EDT 2007
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Application No: 10789355   Version No: 2.0

Input Set:

Output Set:

Started:	2007-09-21 08:46:54.036
Finished:	2007-09-21 08:46:58.740
Elapsed:	0 hr(s) 0 min(s) 4 sec(s) 704 ms
Total Warnings:	30
Total Errors:	0
No. of SeqIDs Defined:	30
Actual SeqID Count:	30

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

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          Input Set:


          Output Set:



          Started:   2007-09-21 08:46:54.036
         Finished:   2007-09-21 08:46:58.740
          Elapsed:   0 hr(s) 0 min(s) 4 sec(s) 704 ms
  Total Warnings:   30
    Total Errors:   0
No. of SeqIDs Defined:   30
  Actual SeqID Count:   30
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Error code   Error Description

This error has occured more than 20 times, will not be displayed

<110> BOEHRINGER INGELHEIM (CANADA) LTD.

<120> SELF REPLICATING RNA MOLECULE FROM
  HEPATITIS C VIRUS

<130> 13/083-3-D2

<140> 10789355
<141> 2004-02-27

<150> 60/257,857
<151> 2000-12-22

<150> 10/029,907
<151> 2001-12-21

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 8639
<212> DNA
<213> HCV

<220>
<221> CDS
<222> (1803)...(8408)

<400> 1

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gtcttcacgc agaaagcgtc tagccatggc gttagtatga gtgtcgtgca gcctccagga  120
cccccccctcc cgggagagcc atagtggtct gcggaaccgg tgagtacacc ggaattgcca  180
ggacgaccgg gtcctttctt ggatcaaccc gctcaatgcc tggagatttg ggcgtgcccc  240
cgcgagactg ctagccgagt agtgttgggt cgcgaaaggc cttgtggtac tgcctgatag  300
ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca ccatgagcac gaatcctaaa  360
cctcaaagaa aaaccaaagg cgcgccatg attgaacaag atggattgca cgcaggttct  420
ccggccgctt gggtggagag gctattcggc tatgactggg cacaacagac aatcggctgc  480
tctgatgccg ccgtgttccg gctgtcagcg caggggcgcc cggttctttt tgtcaagacc  540
gacctgtccg gtgccctgaa tgaactgcag gacgaggcag cgcggctatc gtggctggcc  600
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aaagtatcca tcatggctga tgcaatgcgg cggctgcata cgcttgatcc ggctacctgc  780
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tgcttgccga atatcatggt ggaaaatggc cgcttttctg gattcatcga ctgtggccgg 1020
ctgggtgtgg cggaccgcta tcaggacata gcgttggcta cccgtgatat tgctgaagag 1080
cttggcggcg aatgggctga ccgcttcctc gtgctttacg gtatcgccgc tcccgattcg 1140
cagcgcatcg ccttctatcg ccttcttgac gagttcttct gagttcgcgc ccagatgtta 1200
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gccgaagccg cttggaataa ggccggtgtg cgtttgtcta tatgttattt tccaccatat 1320
tgccgtcttt tggcaatgtg agggcccgga aacctggccc tgtcttcttg acgagcattc 1380
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cc atg gac cgg gag atg gca gca tcg tgc gga ggc gcg gtt ttc gta     1847
   Met Asp Arg Glu Met Ala Ala Ser Cys Gly Gly Ala Val Phe Val
   1               5                   10                  15


ggt ctg ata ctc ttg acc ttg tca ccg cac tat aag ctg ttc ctc gct   1895
Gly Leu Ile Leu Leu Thr Leu Ser Pro His Tyr Lys Leu Phe Leu Ala
              20                  25                  30


agg ctc ata tgg tgg tta caa tat ttt atc acc agg gcc gag gca cac   1943
Arg Leu Ile Trp Trp Leu Gln Tyr Phe Ile Thr Arg Ala Glu Ala His
          35                  40                  45


ttg caa gtg tgg atc ccc ccc ctc aac gtt cgg ggg ggc cgc gat gcc   1991
Leu Gln Val Trp Ile Pro Pro Leu Asn Val Arg Gly Gly Arg Asp Ala
          50                  55                  60


gtc atc ctc ctc acg tgc gcg atc cac cca gag cta atc ttt acc atc   2039
Val Ile Leu Leu Thr Cys Ala Ile His Pro Glu Leu Ile Phe Thr Ile
      65                  70                  75


acc aaa atc ttg ctc gcc ata ctc ggt cca ctc atg gtg ctc cag gct   2087
Thr Lys Ile Leu Leu Ala Ile Leu Gly Pro Leu Met Val Leu Gln Ala
 80                  85                  90                      95


ggt ata acc aaa gtg ccg tac ttc gtg cgc gca cac ggg ctc att cgt   2135
Gly Ile Thr Lys Val Pro Tyr Phe Val Arg Ala His Gly Leu Ile Arg
                  100                 105                 110


gca tgc atg ctg gtg cgg aag gtt gct ggg ggt cat tat gtc caa atg   2183
Ala Cys Met Leu Val Arg Lys Val Ala Gly Gly His Tyr Val Gln Met
              115                 120                 125


gct ctc atg aag ttg gcc gca ctg aca ggt acg tac gtt tat gac cat   2231
Ala Leu Met Lys Leu Ala Ala Leu Thr Gly Thr Tyr Val Tyr Asp His
          130                 135                 140


ctc acc cca ctg cgg gac tgg gcc cac gcg ggc cta cga gac ctt gcg   2279
Leu Thr Pro Leu Arg Asp Trp Ala His Ala Gly Leu Arg Asp Leu Ala
      145                 150                 155


gtg gca gtt gag ccc gtc gtc ttc tct gat atg gag acc aag gtt atc   2327
Val Ala Val Glu Pro Val Val Phe Ser Asp Met Glu Thr Lys Val Ile
160                 165                 170                 175


acc tgg ggg gca gac acc gcg gcg tgt ggg gac atc atc ttg ggc ctg   2375
Thr Trp Gly Ala Asp Thr Ala Ala Cys Gly Asp Ile Ile Leu Gly Leu
                  180                 185                 190


ccc gtc tcc gcc cgc agg ggg agg gag ata cat ctg gga ccg gca gac   2423
Pro Val Ser Ala Arg Arg Gly Arg Glu Ile His Leu Gly Pro Ala Asp
```

agc ctt gaa ggg cag ggg tgg cga ctc ctc gcg cct att acg gcc tac   2471
Ser Leu Glu Gly Gln Gly Trp Arg Leu Leu Ala Pro Ile Thr Ala Tyr
        210   215   220

tcc caa cag acg cga ggc cta ctt ggc tgc atc atc act agc ctc aca   2519
Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr
        225   230   235

ggc cgg gac agg aac cag gtc gag ggg gag gtc caa gtg gtc tcc acc   2567
Gly Arg Asp Arg Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr
240   245   250   255

gca aca caa tct ttc ctg gcg acc tgc gtc aat ggc gtg tgt tgg act   2615
Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr
                260   265   270

gtc tat cat ggt gcc ggc tca aag acc ctt gcc ggc cca aag ggc cca   2663
Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro
        275   280   285

atc acc caa atg tac acc aat gtg gac cag gac ctc gtc ggc tgg caa   2711
Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp Leu Val Gly Trp Gln
        290   295   300

gcg ccc ccc ggg gcg cgt tcc ttg aca cca tgc acc tgc ggc agc tcg   2759
Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser Ser
        305   310   315

gac ctt tac ttg gtc acg agg cat gcc gat gtc att ccg gtg cgc cgg   2807
Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg Arg
320   325   330   335

cgg ggc gac agc agg ggg agc cta ctc tcc ccc agg ccc gtc tcc tac   2855
Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Val Ser Tyr
                340   345   350

ttg aag ggc tct tcg ggc ggt cca ctg ctc tgc ccc tcg ggg cac gct   2903
Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys Pro Ser Gly His Ala
        355   360   365

gtg ggc atc ttt cgg gct gcc gtg tgc acc cga ggg gtt gcg aag gcg   2951
Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys Ala
        370   375   380

gtg gac ttt gta ccc gtc gag tct atg gaa acc act atg cgg tcc ccg   2999
Val Asp Phe Val Pro Val Glu Ser Met Glu Thr Thr Met Arg Ser Pro
        385   390   395

gtc ttc acg gac aac tcg tcc cct ccg gcc gta ccg cag aca ttc cag   3047
Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val Pro Gln Thr Phe Gln
400   405   410   415

gtg gcc cat cta cac gcc cct act ggt agc ggc aag agc act aag gtg   3095
Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val
                420   425   430

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ccg gct gcg tat gca gcc caa ggg tat aag gtg ctt gtc ctg aac ccg    3143
Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro
        435             440             445

tcc gtc gcc gcc acc cta ggt ttc ggg gcg tat atg tct aag gca cat    3191
Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His
        450             455             460

ggt atc gac cct aac atc aga acc ggg gta agg acc atc acc acg ggt    3239
Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly
        465             470             475

gcc ccc atc acg tac tcc acc tat ggc aag ttt ctt gcc gac ggt ggt    3287
Ala Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly
480             485             490             495

tgc tct ggg ggc gcc tat gac atc ata ata tgt gat gag tgc cac tca    3335
Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser
            500             505             510

act gac tcg acc act atc ctg ggc atc ggc aca gtc ctg gac caa gcg    3383
Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala
            515             520             525

gag acg gct gga gcg cga ctc gtc gtg ctc gcc acc gct acg cct ccg    3431
Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro
        530             535             540

gga tcg gtc acc gtg cca cat cca aac atc gag gag gtg gct ctg tcc    3479
Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser
        545             550             555

agc act gga gaa atc ccc ttt tat ggc aaa gcc atc ccc atc gag acc    3527
Ser Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Thr
560             565             570             575

atc aag ggg ggg agg cac ctc att ttc tgc cat tcc aag aag aaa tgt    3575
Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys
            580             585             590

gat gag ctc gcc gcg aag ctg tcc ggc ctc gga ctc aat gct gta gca    3623
Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Leu Asn Ala Val Ala
        595             600             605

tat tac cgg ggc ctt gat gta tcc gtc ata cca act agc gga gac gtc    3671
Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val
        610             615             620

att gtc gta gca acg gac gct cta atg acg ggc ttt acc ggc gat ttc    3719
Ile Val Val Ala Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe
        625             630             635

gac tca gtg atc gac tgc aat aca tgt gtc acc cag aca gtc gac ttc    3767
Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe
640             645             650             655
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agc ctg gac ccg acc ttc acc att gag acg acg acc gtg cca caa gac        3815
Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp
            660             665             670

gcg gtg tca cgc tcg cag cgg cga ggc agg act ggt agg ggc agg atg        3863
Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Met
            675             680             685

ggc att tac agg ttt gtg act cca gga gaa cgg ccc tcg ggc atg ttc        3911
Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe
            690             695             700

gat tcc tcg gtt ctg tgc gag tgc tat gac gcg ggc tgt gct tgg tac        3959
Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr
            705             710             715

gag ctc acg ccc gcc gag acc tca gtt agg ttg cgg gct tac cta aac        4007
Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn
720             725             730             735

aca cca ggg ttg ccc gtc tgc cag gac cat ctg gag ttc tgg gag agc        4055
Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser
            740             745             750

gtc ttt aca ggc ctc acc cac ata gac gcc cat ttc ttg tcc cag act        4103
Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr
            755             760             765

aag cag gca gga gac aac ttc ccc tac ctg gta gca tac cag gct acg        4151
Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr
            770             775             780

gtg tgc gcc agg gct cag gct cca cct cca tcg tgg gac caa atg tgg        4199
Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp
            785             790             795

aag tgt ctc ata cgg cta aag cct acg ctg cac ggg cca acg ccc ctg        4247
Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu
800             805             810             815

ctg tat agg ctg gga gcc gtt caa aac gag gtt act acc aca cac ccc        4295
Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Thr Thr His Pro
            820             825             830

ata acc aaa tac atc atg gca tgc atg tcg gct gac ctg gag gtc gtc        4343
Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val
            835             840             845

acg agc acc tgg gtg ctg gta ggc gga gtc cta gca gct ctg gcc gcg        4391
Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala
            850             855             860

tat tgc ctg aca aca ggc agc gtg gtc att gtg ggc agg atc atc ttg        4439
Tyr Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
            865             870             875

tcc gga aag ccg gcc atc att ccc gac agg gaa gtc ctt tac cgg gag        4487
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Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu
880             885             890             895

ttc gat gag atg gaa gag tgc gcc tca cac ctc cct tac atc gaa cag   4535
Phe Asp Glu Met Glu Glu Cys Ala Ser His Leu Pro Tyr Ile Glu Gln
            900             905             910

gga atg cag ctc gcc gaa caa ttc aaa cag aag gca atc ggg ttg ctg   4583
Gly Met Gln Leu Ala Glu Gln Phe Lys Gln Lys Ala Ile Gly Leu Leu
            915             920             925

caa aca gcc acc aag caa gcg gag gct gct gct ccc gtg gtg gaa tcc   4631
Gln Thr Ala Thr Lys Gln Ala Glu Ala Ala Ala Pro Val Val Glu Ser
        930             935             940

aag tgg cgg acc ctc gaa gcc ttc tgg gcg aag cat atg tgg aat ttc   4679
Lys Trp Arg Thr Leu Glu Ala Phe Trp Ala Lys His Met Trp Asn Phe
        945             950             955

atc agc ggg ata caa tat tta gca ggc ttg tcc act ctg cct ggc aac   4727
Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu Pro Gly Asn
960             965             970             975

ccc gcg ata gca tca ctg atg gca ttc aca gcc tct atc acc agc ccg   4775
Pro Ala Ile Ala Ser Leu Met Ala Phe Thr Ala Ser Ile Thr Ser Pro
            980             985             990

ctc acc acc caa cat acc ctc ctg ttt aac atc ctg ggg gga tgg gtg   4823
Leu Thr Thr Gln His Thr Leu Leu Phe Asn Ile Leu Gly Gly Trp Val
            995             1000            1005

gcc gcc caa ctt gct cct ccc agc gct gct tct gct ttc gta ggc gcc   4871
Ala Ala Gln Leu Ala Pro Pro Ser Ala Ala Ser Ala Phe Val Gly Ala
            1010            1015            1020

ggc atc gct gga gcg gct gtt ggc agc ata ggc ctt ggg aag gtg ctt   4919
Gly Ile Ala Gly Ala Ala Val Gly Ser Ile Gly Leu Gly Lys Val Leu
            1025            1030            1035

gtg gat att ttg gca ggt tat gga gca ggg gtg gca ggc gcg ctc gtg   4967
Val Asp Ile Leu Ala Gly Tyr Gly Ala Gly Val Ala Gly Ala Leu Val
1040            1045            1050            1055

gcc ttt aag gtc atg agc ggc gag atg ccc tcc acc gag gac ctg gtt   5015
Ala Phe Lys Val Met Ser Gly Glu Met Pro Ser Thr Glu Asp Leu Val
            1060            1065            1070

aac cta ctc cct gct atc ctc tcc cct ggc gcc cta gtc gtc ggg gtc   5063
Asn Leu Leu Pro Ala Ile Leu Ser Pro Gly Ala Leu Val Val Gly Val
            1075            1080            1085

gtg tgc gca gcg ata ctg cgt cgg cac gtg ggc cca ggg gag ggg gct   5111
Val Cys Ala Ala Ile Leu Arg Arg His Val Gly Pro Gly Glu Gly Ala
            1090            1095            1100

gtg cag tgg atg aac cgg ctg ata gcg ttc gct tcg cgg ggt aac cac   5159
Val Gln Trp Met Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His
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gtc tcc ccc acg cac tat gtg cct gag agc gac gct gca gca cgt gtc   5207
Val Ser Pro Thr His Tyr Val Pro Glu Ser Asp Ala Ala Ala Arg Val
1120   1125   1130   1135

act cag atc ctc tct agt ctt acc atc act cag ctg ctg aag agg ctt   5255
Thr Gln Ile Leu Ser Ser Leu Thr Ile Thr Gln Leu Leu Lys Arg Leu
                    1140   1145   1150

cac cag tgg atc aac gag gac tgc tcc acg cca tgc tcc ggc tcg tgg   5303
His Gln Trp Ile Asn Glu Asp Cys Ser Thr Pro Cys Ser Gly Ser Trp
                1155   1160   1165

cta aga gat gtt tgg gat tgg ata tgc acg gtg ttg act gat ttc aag   5351
Leu Arg Asp Val Trp Asp Trp Ile Cys Thr Val Leu Thr Asp Phe Lys
            1170   1175   1180

acc tgg ctc cag tcc aag ctc ctg ccg cga ttg ccg gga gtc ccc ttc   5399
Thr Trp Leu Gln Ser Lys Leu Leu Pro Arg Leu Pro Gly Val Pro Phe
        1185   1190   1195

ttc tca tgt caa cgt ggg tac aag gga gtc tgg cgg ggc gac ggc atc   5447
Phe Ser Cys Gln Arg Gly Tyr Lys Gly Val Trp Arg Gly Asp Gly Ile
1200   1205   1210   1215

atg caa acc acc tgc cca tgt gga gca cag atc acc gga cat gtg aaa   5495
Met Gln Thr Thr Cys Pro Cys Gly Ala Gln Ile Thr Gly His Val Lys
                    1220